

AMENDMENT TO THE CLAIMS

The following list of claims replaces all prior claims of the application.

1. (Previously presented) An isolated nucleic acid molecule consisting essentially of the nucleic acid sequence of SEQ ID NO:2471, 2472, or a complement thereof, wherein said nucleic acid molecule is 100 nucleotides or less in length.
2. (Previously presented) An isolated nucleic acid molecule consisting essentially of the nucleic acid sequence of SEQ ID NO:2474, 2475, or a complement thereof, wherein said nucleic acid molecule is 100 nucleotides or less in length.
3. (Currently amended) An isolated nucleic acid molecule consisting essentially of the nucleic acid sequence of SEQ ID NO:2473[[, 2476]], or a complement thereof, wherein said nucleic acid molecule is 100 nucleotides or less in length.
- 4-10. (Cancelled).
11. (Currently amended) A method for detecting the presence of the hSARS virus in a biological sample, said method comprising:
 - (a) ~~amplifying a nucleic acid of the hSARS virus from said sample~~ using primers, one of which consists of the nucleic acid sequence of SEQ ID NOS:2471 or 2472; [[and]]
 - (b) detecting in the nucleic acid using a probe consisting of the nucleic acid sequence of SEQ ID NO:2473; and
 - (c) wherein said detecting indicates the presence of the hSARS virus in said sample.
12. (Currently amended) A method for detecting the presence of the hSARS virus in a biological sample, said method comprising:

(a) amplifying a nucleic acid ~~of the hSARS virus~~ from said sample using primers, one of which consists of the nucleic acid sequence of SEQ ID NOS:2474 or 2475; ~~[[and]]~~

(b) detecting in the nucleic acid using a probe consisting of the nucleic acid sequence of SEQ ID NO:2476; and

(c) wherein said detecting indicates the presence of the hSARS virus in said sample.

13. (Currently amended) A method for identifying a subject infected with the hSARS virus, said method comprising:

(a) obtaining total RNA from a biological sample obtained from the subject;

(b) reverse transcribing the total RNA to obtain cDNA; and

(c) subjecting the cDNA to PCR assay using a set of primers derived from a nucleotide sequence of the hSARS virus having China Center for Type Culture Collection Deposit Accession No. CCTCC-V200303;

(d) detecting a product of PCR assay; and

(e) wherein said detecting indicates that the subject is infected with hSARS virus.

14. (Currently amended) A method for identifying a subject infected with the hSARS virus, said method comprising:

(a) obtaining total RNA from a biological sample obtained from the subject

(b) reverse transcribing the total RNA to obtain cDNA; ~~[[and]]~~

- (c) subjecting the cDNA to PCR assay using a set of primers, one of which consists of the nucleic acid sequence of SEQ ID NOS:2471 or 2472;
- (d) detecting a product of PCR assay; and
- (e) wherein said detecting indicates that the subject is infected with hSARS virus.

15. (Currently amended) The method of claim 14, ~~further comprising (d) detecting a product of PCR assay~~ wherein said product in step (d) is detected with a probe.

16. (Previously presented) The method of claim 15, wherein the probe is a nucleic acid molecule consisting of the nucleotide sequence of SEQ ID NO:2473.

17. (Currently amended) A method for identifying a subject infected with the hSARS virus, said method comprising:

- (a) obtaining total RNA from a biological sample obtained from the subject
- (b) reverse transcribing the total RNA to obtain cDNA; [[and]]
- (c) subjecting the cDNA to PCR assay using a set of primers, one of which consists of the nucleic acid sequence of SEQ ID NOS:2474 or 2475;
- (d) detecting a product of PCR assay; and
- (e) wherein said detecting indicates that the subject is infected with hSARS virus.

18. (Currently amended) The method of claim 17, ~~further comprising (d) detecting a product of PCR assay~~ wherein said product in step (d) is detected with a probe.

19. (Previously presented) The method of claim 18, wherein the probe is a nucleic acid molecule consisting of the nucleotide sequence of SEQ ID NO:2476.

20. (Previously presented) A kit comprising in one or more containers one or more isolated nucleic acid molecules consisting essentially of a nucleotide sequence selected from the group consisting of SEQ ID NO:2471, SEQ ID NO:2472, and SEQ ID NO:2473, wherein the nucleic acid molecule or molecules are 100 nucleotides or less in length.

21. (Currently amended) A kit comprising in one or more containers a polymerase and one or more isolated nucleic acid molecules consisting essentially of a nucleotide sequence selected from the group consisting of SEQ ID NO:2474, SEQ ID NO:2475, and SEQ ID NO:2476, wherein the nucleic acid molecule or molecules are 100 nucleotides or less in length.

22. (Currently amended) An isolated nucleic acid molecule consisting essentially of at least ~~[[10]]~~ 15 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:2471, 2472, or a complement thereof, wherein said nucleic acid molecule is 100 nucleotides or less in length.

23. (Currently amended) An isolated nucleic acid molecule consisting essentially of at least ~~[[10]]~~ 15 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:2474, 2475, or a complement thereof, wherein said nucleic acid molecule is 100 nucleotides or less in length.

24 (Currently amended) An isolated nucleic acid molecule consisting essentially of at least ~~[[10]]~~ 15 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:2473~~[[, 2476]]~~, or a complement thereof, wherein said nucleic acid molecule is 100 nucleotides or less in length.

25. (Currently amended) A method for identifying a subject infected with the hSARS virus, said method comprising:

- (a) obtaining total RNA from a biological sample obtained from the subject
- (b) reverse transcribing the total RNA to obtain cDNA; and
- (c) subjecting the cDNA to PCR assay using a set of primers, one of which is ~~[[the]]~~ a nucleic acid molecule according to claim 22 consisting essentially of at least 10 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:2471, 2472, or a complement thereof;
- (d) detecting a product of PCR assay; and
- (e) wherein said detecting indicates that the subject is infected with hSARS virus.

26. (Currently amended) The method of claim 25, ~~further comprising (d) detecting a product of PCR assay~~ wherein said product in step (d) is detected with a probe.

27. (Currently amended) The method of claim 26, wherein the probe is a nucleic acid molecule consisting essentially of at least 10 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:2473 ~~and is 100 nucleotides or less in length.~~

28. (Currently amended) A method for identifying a subject infected with the hSARS virus, said method comprising:

- (a) obtaining total RNA from a biological sample obtained from the subject
- (b) reverse transcribing the total RNA to obtain cDNA; and

(c) subjecting the cDNA to PCR assay using a set of primers, one of which is ~~[[the]]~~ a nucleic acid molecule according to claim 23 consisting essentially of at least 10 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:2474, 2475, or a complement thereof;

(d) detecting a product of PCR assay; and

(e) wherein said detecting indicates that the subject is infected with hSARS virus.

29. (Currently amended) The method of claim 28 ~~further comprising (d) detecting a product of PCR assay~~ wherein said product in step (d) is detected with a probe.

30. (Currently amended) The method of claim 29, wherein the probe is a nucleic acid molecule consisting essentially of at least 10 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:2476 ~~and is 100 nucleotides or less in length.~~

31. (New) An isolated nucleic acid molecule consisting essentially of at least 15 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:2476, or a complement thereof, wherein said nucleic acid molecule is from 25 to 100 nucleotides inclusive in length.

32. (New) A kit comprising in one or more containers one or more isolated nucleic acid molecules consisting essentially of a nucleotide sequence selected from the group consisting of SEQ ID NO:2474 and SEQ ID NO:2475, wherein the nucleic acid molecule or molecules are 100 nucleotides or less in length.